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The chestnut pathogen *Gnomoniopsis smithogilvyi* (*Gnomoniaceae*, *Diaporthales*) and its synonyms

Lucas A. Shuttleworth [1], Donald M. Walker [2,3] & David I. Guest [1*]

[1]*Faculty of Agriculture and Environment, University of Sydney, 1 Central Avenue, Australian Technology Park, Eveleigh NSW 2015, Australia*

[2]*Department of Natural Sciences, The University of Findlay, 1000 North Main St., Findlay, OH 45840, U.S.A.*

[3] *Department of Biology, Tennessee Tech University, 1100 N. Dixie Avenue, Cookeville TN 38505, U.S.A.*

* Correspondence to: *david.guest@sydney.edu.au*

Abstract — Two species, *Gnomoniopsis smithogilvyi* and *G. castaneae*, were described independently in 2012 as causal agents of chestnut (*Castanea*) rot in Australasia and Europe. A comparative morphological analysis and five-marker phylogenetic analysis of ITS, TEF1-α, β-tubulin, MS204, and FG1093 confirm that both names refer to the same species, and an investigation of their exact publication dates demonstrates that *G. smithogilvyi* has priority over *G. castaneae.*

Key words — canker, endophyte, *Gnomonia*, nut rot

Introduction

Species of *Gnomoniopsis* have a mainly northern hemisphere distribution and are economically important pathogens of the rosaceous hosts blackberry, raspberry, and strawberry (Bolay 1971, Monod 1983, Maas 1998, Sogonov et al. 2008, Walker et al. 2010).

Shuttleworth et al. (2012a) described a new species, *Gnomoniopsis smithogilvyi,* as the causal agent of chestnut rot, as an endophyte of reproductive and vegetative tissues, and as a saprobe of European chestnut (*Castanea sativa* Mill.) and hybrids of Japanese chestnut and European chestnut (*Castanea crenata* Siebold & Zucc. × *C. sativa)* in southeastern Australia (Shuttleworth et al. 2012a,b). Shuttleworth et al. (2012a) also found *G. smithogilvyi* occurring in New Zealand on *C. crenata, C. sativa,* and *Castanea* sp. and associated with *C. sativa* in India and Italy.

Visentin et al. (2012) described a new species, *Gnomoniopsis castaneae* [as "*castanea*"], as the causal agent of nut rot, endophyte, and saprobe of *C. sativa* in France, Italy, New Zealand, and Switzerland. They referred to the fungus reported earlier as a *Gnomonia* sp. (informally named *"G. pascoe"*) as the main causal agent of chestnut rot in Australia and New Zealand (Smith & Ogilvy 2008). Sequences from Swiss isolates have been deposited as *G. castaneae* (Dennert et al. 2014), and an Italian isolate from necrosis of insect-induced galls of *Castanea* has also been identified as *G. castaneae* (Vinale et al. 2014).

The aim of this paper is to clarify the taxonomic relationship of *G. smithogilvyi* and *G. castaneae* and, if they are conspecific, to determine which name has priority.

Materials & methods

Morphology

Observation of cultures of *G. smithogilvyi* CBS 130190 (ex-type) from Australia, *G. castaneae* MUT 401 (ex-type) from Italy, and "*Gnomonia pascoe*" MUT 411 from New Zealand were made from herbarium material. Herbarium specimens of the sexual phase were not examined in this study.

Sequencing and phylogenetic analyses

Fragments of four protein coding markers TEF1-α, β-tubulin, MS204, FG1093 were amplified and sequenced for *Gnomoniopsis smithogilvyi* CBS 130190 (ex-type), CBS 130188 and CBS 130189, *G. castaneae* MUT 401 (ex-type) and "*Gnomonia pascoe*" MUT 411 using primer pairs TEF1-α: EF1-728F (Carbone & Kohn 1999)/EF1-1567 (Rehner 2001), β-tubulin: T1/T2 (O'Donnell & Cigelnik 1997), MS204: amplification E1F1/E5R1, sequencing E3F1/E4R1a/E5R1a, FG1093: ElFla/E3Rla (all MS204 and FG1093 primers; Walker et al. 2012).

Thermocycling conditions were identical to Walker et al. (2010, 2012). In addition, ITS sequences and reference sequences were downloaded from GenBank (Table 1). Alignments were completed with the MAFFT alignment option (Katoh et al. 2002) of Geneious® R7 v7.1.2 (Biomatters Ltd., New Zealand) with default settings applied. Six alignments were completed, one for each of the five individual marker datasets and one for the combined five-marker dataset.

For the TEF1-α, β-tubulin, MS204, FG1093 and the combined five-marker dataset, nineteen isolates were selected including reference species of *Gnomoniopsis*. The ITS analyses included an addition four isolates from India, six from Italy, two from France, six from New Zealand, and two from Switzerland. Sequences from studies in India and Switzerland associated with cankers of *C. sativa* were also included (Dar & Rai 2013, 2015, Pasche et al. 2015).

Two outgroup isolates were selected based on Walker et al. (2012), specifically *Ophiognomonia setacea* CBS 128354 and *Plagiostoma* sp. CBS 128351. *Gnomoniopsis guttulata* was excluded from the five-marker dataset because sequences for four of the five markers were not available. Although MS204 and FG1093 sequences were not available for *G. racemula,* this taxon was included in the five-marker dataset.

Table 1. GenBank accessions and country of collection for *Gnomoniopsis* and outgroup isolates used in the phylogenetic analyses to delineate *G. smithogilvyi* and its synonyms.

Species	Isolate	Country	GenBank accessions				
			ITS	TEF1-α	β-tubulin	MS204	FG1093
G. alderdunensis	CBS 125680	U.S.A.	GU320825	GU320801	GU320787	JF319036	JF274653
G. chamaemori	CBS 804.79	Finland	GU320817	GU320809	GU320777	JF319029	JF274646
G. clavulata	CBS 121255	U.S.A.	EU254818	GU320807	EU219211	JF319027	JF274644
G. comari	CBS 806.79	Finland	EU254821	GU320810	EU219156	JF319030	JF274647
G. fructicola	CBS 208.34	France	EU254826	GU320808	EU219149	JF319028	JF274645
G. guttulata	MS 0312	Bulgaria	EU254812	–	–	–	–
G. idaeicola	CBS 125676	U.S.A.	GU320821	GU320811	GU320784	JF319037	JF274654
G. macounii	CBS 121468	U.S.A.	EU254762	GU320804	EU219126	JF319024	JF274641
G. occulta	CBS 125678	U.S.A.	GU320829	GU320800	GU320786	JF319033	JF274650
G. paraclavulata	CBS 123202	U.S.A.	GU320830	GU320815	GU320775	JF319025	JF274642
G. racemula	CBS 121469	U.S.A.	EU254841	GU320803	EU219125	–	–
G. sanguisorbae	CBS 858.79	Switzerland	GU320818	GU320805	GU320790	JF319031	JF274648
G. smithogilvyi	CBS 130190	Australia	JQ910642	**KR072534**	JQ910639	**KR072539**	**KR072544**
	CBS 130189	Australia	JQ910644	**KR072535**	JQ910641	**KR072540**	**KR072545**
	CBS 130188	Australia	JQ910643	**KR072536**	JQ910640	**KR072541**	**KR072546**
	LSV908	France	KJ173703	—	—	—	—
	MUT 815	France	JQ898298	NU	—	—	—
	Gn_TN5	Italy	JX094888	—	—	—	—
	MUT 401	Italy	HM142946	**KR072537**	**KR072532**	**KR072542**	**KR072547**
	M4perDA	Italy	JN793531	—	—	—	—
	M3Cu	Italy	JN793534	—	—	—	—

Concluded on p. 932

Table 1, concluded

Species	Isolate	Country	GenBank accessions				
			ITS	TEF1-α	β-tubulin	MS204	FG1093
(*G. smithogilvyi*, continued)	M6EmA	Italy	JN793535	—	—	—	—
	Gm_TN1	Italy	JX094889	—	—	—	—
	Gm_TO	Italy	JX094892	—	—	—	—
	AU/DBT305	India	KC963938	—	—	—	—
	AU/DBT306	India	KC963940	—	—	—	—
	AU/DBT296	India	KC963944	—	—	—	—
	INDC(BSF5)A	India	JQ268073	—	—	—	—
	MUT 411	New Zealand	HM1142948	**KR072538**	**KR072533**	**KR072543**	**KR072548**
	ICMP:14492	New Zealand	KC145967	NU	—	—	—
	ICMP:14080	New Zealand	KC145870	NU	—	—	—
	CBS 121477	New Zealand	EU254854	—	—	—	—
	CBS 121917	New Zealand	EU254851	NU	—	—	—
	CBS 121918	New Zealand	EU254855	NU	NU	—	—
	MUT 810	Switzerland	JQ898295	NU	—	—	—
	Ge1	Switzerland	KP824754	NU	NU	—	—
G. tormentillae	CBS 904.79	Switzerland	EU254856	GU320795	EU219165	JF319032	JF274649
Ophiognomonia setacea	CBS 128354	U.S.A.	JF514847	JF514823	JF514839	JF319035	JF274652
Plagiostoma sp.	CBS 128351	U.S.A.	JF514852	JF514833	JF514836	JF319034	JF274651

One isolate per reference species was selected. GenBank accessions for sequences generated in the current study are in bold. AU and IND = isolates associated with Dar & Rai (2013); CBS = Centraalbureau voor Schimmelcultures, Utrecht, the Netherlands; Ge1 = isolate associated with Pasche et al. (2015); Gm and Gn = isolates associated with Maresi et al. (2013); ICMP = International Collection of Micro-organisms from Plants, Landcare Research, Auckland, New Zealand; MS = isolate associated with Sogonov et al. (2008); MUT = Mycotheca Universitatis Taurinensis, University of Turin, Italy. Other isolates downloaded as sequences from unpublished work.

Two criteria were used for phylogenetic species recognition: genealogical concordance phylogenetic species recognition (GCPSR; Taylor et al. 2000) and the genealogical sorting index (GSI; Cummings et al. 2008). A conditional comparison test to determine GCPSR was completed to identify support for the *G. smithogilvyi* clade on the individual marker datasets using maximum parsimony bootstrap support (MPBS) ≥70% (Mason-Gamer & Kellogg 1996, Kellogg et al. 1996). The GSI is a statistical measure to determine if predefined groups on a phylogenetic tree have reached reciprocal monophyly thus sharing exclusive ancestry. It is interpreted on a 0 to 1 continuum where 0 = lack of genealogical divergence from other groups and 1 = monophyly (Cummings et al. 2008). All five single marker and the combined marker alignments were independently tested with GSI using 100 randomly selected trees calculated from the GARLI maximum likelihood bootstrap (MLBS) tree distribution computed with the GARLI (v2.1) web service hosted at molecularevolution.org (Bazinet et al. 2014, Zwickl 2006). The GSI analyses were performed with a web service hosted at molecularevolution.org (GSI v0.92; Cummings et al. 2008) using 10,000 permutations to determine statistical significance (*P*-value ≤0.05). Independent GSI values from the MLBS tree distribution were pooled to calculate an ensemble statistic GSI_T for each marker and the combined marker alignment (Table 2).

Table 2. Phylogenetic species recognition of *Gnomoniopsis smithogilvyi*

Marker	GCPSR (MPBS %)	gsi_T	p-value
ITS	99	1	0.0001
TEF1-α	100	1	0.0001
β-tubulin	100	1	0.0005
MS204	100	1	0.0001
FG1093	100	1	0.0003
Concatenated dataset	100	1	0.0001

Maximum parsimony bootstrap support (MPBS) ≥70% indicates strong support for the *G. smithogilvyi* clade. The gene sorting index (GSI) is based on a 0 to 1 continuum, 0 = lack of genealogical divergence from other groups and 1 = monophyly; p-values ≤0.05 indicate the GSI is statistically significant.

Maximum parsimony (MP), maximum likelihood (ML), and Bayesian analyses were used to infer phylogenetic trees. MP and ML trees were inferred with MEGA6 (Tamura et al. 2013). The Bayesian trees were inferred with MRBAYES (Huelsenbeck & Ronquist 2001). The MP analyses used the heuristic search option with 1000 random sequence addition replicates, the tree-bisection reconnection (TBR) branch-swapping option with MULTTREES on, and MAXTREES set at 1000. All characters had equal weight. For the ML and Bayesian analyses, jModeltest 2.1 (Posada 2008) was used to determine the optimal model that best fit the individual marker and the five-marker datasets. The resulting model was GTR+I+G for all datasets.

Branch support in ML and MP analyses were determined with maximum likelihood bootstrap (MLBS) and maximum parsimony bootstrap (MPBS) analyses in MEGA6. The MLBS and MPBS were calculated using 1000 bootstrap replicates, with 10 random addition replicates per bootstrap replicate in the MPBS analysis (Felsenstein 1985). A threshold of ≥70% support was used as a cut-off for strongly supported tree nodes for both MPBS and MLBS. The Bayesian analyses used the Markov Chain Monte Carlo (MCMC) method. Identical nucleotide substitution models were used ML and Bayesian analyses. Four heated chains were run with 5 million generations, a subsampling frequency of 2000 generations and a burn-in of 500,000 generations (10%).

Results & discussion

Morphology

Measurements of asexual culture characters agreed with the published descriptions of Shuttleworth et al. (2012a) and Visentin et al. (2012). However, conidia of all isolates were hyaline and mostly multi-guttulate (although occasionally uni- and bi-guttulate). The differences in the published descriptions of the sexual states were the biseriate arrangement of ascospores in *G. smithogilvyi* (Shuttleworth et al. 2012a) and the uniseriate or irregularly multiseriate arrangement in *G. castaneae* (Visentin et al. 2012).

Morphologically, the sexual states of *Gnomoniopsis* spp. are characterised by small black perithecia that are immersed in host tissue, solitary, lacking a stroma or in groups aggregated in a minimal stroma, with a single central, marginal or lateral neck (Sogonov et al. 2008). Asci are oval to fusiform with a visible apical ring and contain eight spores. The ascospores are one-septate, oval to fusiform, and without appendages (except in *G. tormentillae;* Barr 1978). The known asexual states of *Gnomoniopsis* have subglobose pycnidia with one-celled hyaline conidia that are oval, oblong, globose or femur-shaped. *Gnomoniopsis smithogilvyi* fits morphologically into this description of *Gnomoniopsis.*

Gnomoniopsis smithogilvyi can be separated morphologically from its sister species *G. paraclavulata* Sogonov and *G. clavulata* (Ellis) Sogonov by having smaller ascospores (*G. smithogilvyi* mean length × width = 7 µm × 2 µm [(Shuttleworth et al. 2012a); *G. paraclavulata* 9.5 µm × 3.5 µm (Sogonov et al. 2008); *G. clavulata* 9 µm × 4 µm (Sogonov et al. 2008)].

Host range

Most *Gnomoniopsis* species show host specificity to genera in *Fagaceae*, *Onagraceae*, or *Rosaceae* (Walker et al. 2010). *Gnomoniopsis smithogilvy*i, *G. paraclavulata,* and *G. clavulata* can be separated by their known host ranges. All three species are reported on fagaceous hosts, but *Gnomoniopsis smithogilvyi* is reported only on *Castanea* spp., *G. paraclavulata* is reported only on *Quercus* spp., and *G. clavulata* is reported on *Fagus sylvatica* and *Quercus* spp. (Sogonov et al. 2008).

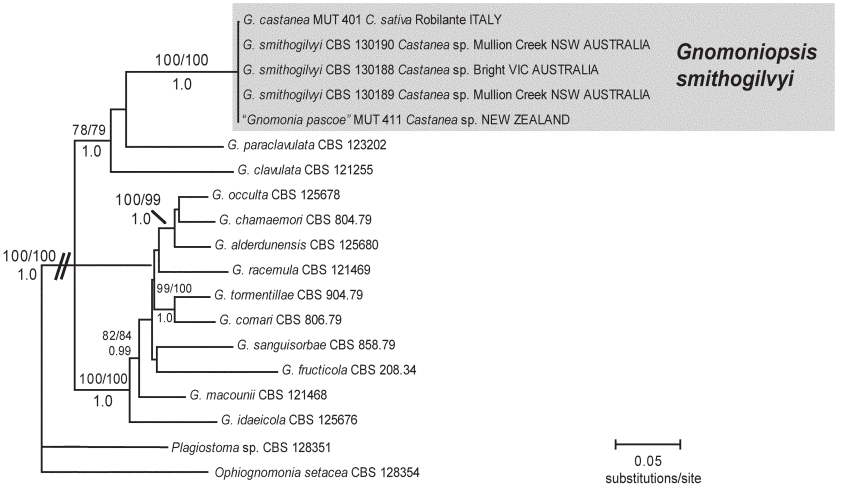

Fig. 1. ML phylogeny of combined ITS/TEF1-α/β-tubulin/MS204/FG1093 sequences of *G. smithogilvyi*, *G. castanea*, and "*G. pascoe*", with single isolates of *Gnomoniopsis* reference taxa and outgroup (ML score = –lnL score of 16532.47). Maximum likelihood bootstrap (MLBS), maximum parsimony bootstrap (MPBS) values ≥70%, and Bayesian posterior probabilities (PP) ≥0.95 are displayed at each branch in the order MLBS/MPBS/PP.

Phylogenetic analyses

The alignment lengths for the six datasets including gaps were ITS: 508 bp, TEF1-α: 917 bp, β-tubulin: 593 bp, MS204: 774 bp, FG1093: 351 bp, and the combined five-marker: 3137 bp. The topology of the ML five-marker phylogeny grouped *Gnomoniopsis* isolates from *Castanea* in Australia, Italy and New Zealand in the same strongly supported lineage (MLBS = 100%; Fig. 1). Of the 3137 total-character MP five-marker dataset, 763 were parsimony informative, 471 parsimony uninformative, and 1903 constant. The MP heuristic search produced three most parsimonious trees of 2717 steps (CI = 0.687523, RI = 0.701477, RCI = 0.482281 for all sites, and iCI = 0.601034, iRI = 0.701477, iRCI = 0.421611 for parsimony informative sites). The topology of the MP five-marker phylogeny was similar to the ML phylogeny, grouping *Gnomoniopsis* isolates from *Castanea* in Australia, Italy, and New Zealand in the same strongly supported lineage (MPBS = 100%). The most likely ML five-marker tree had –lnL score 16532.47. The Bayesian distribution of likelihood scores was –lnL 16403.508–16414.583, and the PP of the branch supporting the isolates from *Castanea* was 1.00.

The ML ITS analysis resulted in a most likely tree with a –lnL score of 1866.45. Twenty-five isolates from *Castanea* collected in Australia, France, India, Italy,

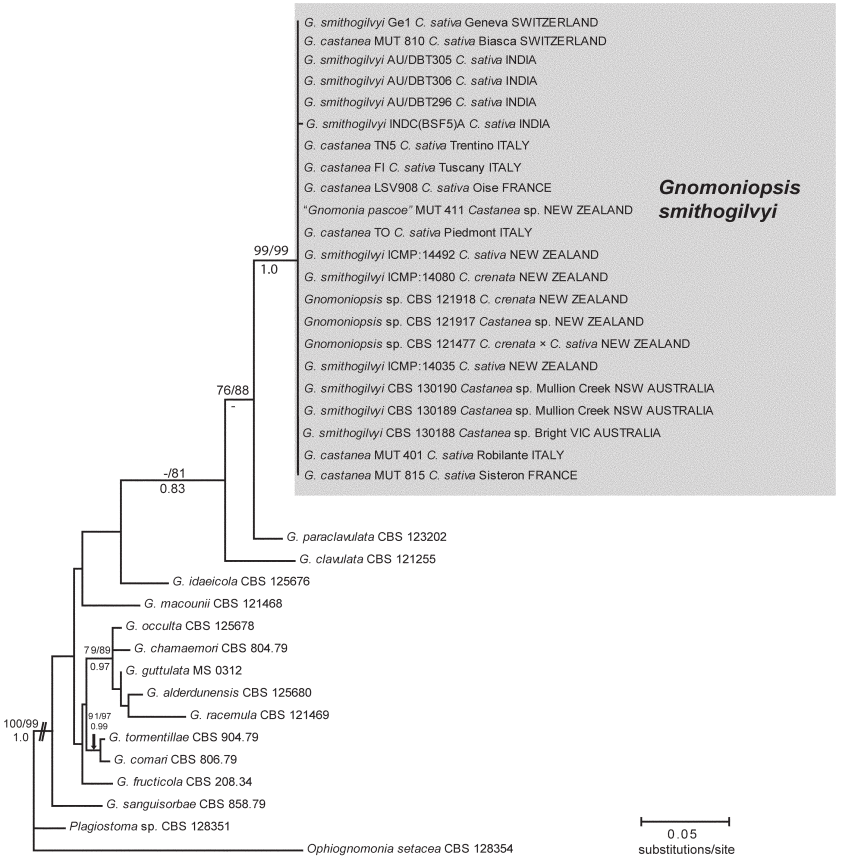
G. smithogilvyi Ge1 C. sativa Geneva SWITZERLAND
G. castanea MUT 810 C. sativa Biasca SWITZERLAND
G. smithogilvyi AU/DBT305 C. sativa INDIA
G. smithogilvyi AU/DBT306 C. sativa INDIA
G. smithogilvyi AU/DBT296 C. sativa INDIA
G. smithogilvyi INDC(BSF5)A C. sativa INDIA
G. castanea TN5 C. sativa Trentino ITALY
G. castanea FI C. sativa Tuscany ITALY
G. castanea LSV908 C. sativa Oise FRANCE
"Gnomonia pascoe" MUT 411 Castanea sp. NEW ZEALAND
G. castanea TO C. sativa Piedmont ITALY
G. smithogilvyi ICMP:14492 C. sativa NEW ZEALAND
G. smithogilvyi ICMP:14080 C. crenata NEW ZEALAND
Gnomoniopsis sp. CBS 121918 C. crenata NEW ZEALAND
Gnomoniopsis sp. CBS 121917 Castanea sp. NEW ZEALAND
Gnomoniopsis sp. CBS 121477 C. crenata × C. sativa NEW ZEALAND
G. smithogilvyi ICMP:14035 C. sativa NEW ZEALAND
G. smithogilvyi CBS 130190 Castanea sp. Mullion Creek NSW AUSTRALIA
G. smithogilvyi CBS 130189 Castanea sp. Mullion Creek NSW AUSTRALIA
G. smithogilvyi CBS 130188 Castanea sp. Bright VIC AUSTRALIA
G. castanea MUT 401 C. sativa Robilante ITALY
G. castanea MUT 815 C. sativa Sisteron FRANCE
Gnomoniopsis smithogilvyi
99/99
1.0
76/88
-
-/81
0.83
G. paraclavulata CBS 123202
G. clavulata CBS 121255
G. idaeicola CBS 125676
G. macounii CBS 121468
G. occulta CBS 125678
79/89
0.97
G. chamaemori CBS 804.79
G. guttulata MS 0312
G. alderdunensis CBS 125680
91/97
0.99
G. racemula CBS 121469
100/99
1.0
G. tormentillae CBS 904.79
G. comari CBS 806.79
G. fructicola CBS 208.34
G. sanguisorbae CBS 858.79
Plagiostoma sp. CBS 128351
Ophiognomonia setacea CBS 128354
0.05
substitutions/site

Fig. 2. ML phylogeny of ITS sequences of *G. smithogilvyi*, *G. castanea*, and "*G. pascoe*" with single isolates of *Gnomoniopsis* reference taxa and outgroup (ML score = –lnL score of 1866.45). Country of collection, and species of *Castanea* that the isolate was collected from are next to the isolate number. Maximum likelihood bootstrap (ML), maximum parsimony bootstrap (MP) values ≥70%, and Bayesian posterior probabilities (PP) ≥0.95 are displayed at each branch in the order MLBS/MPBS/PP.

New Zealand, and Switzerland clustered in the same lineage with 99% MLBS support (Fig. 2). One isolate from France, LSV908, displayed minor interspecific variation with 1 bp different from the other isolates from *Castanea*. The MP ITS dataset had 508 total characters: 68 parsimony informative, 56 parsimony uninformative, and 384 constant. The MP heuristic search produced three most parsimonious trees with length of 228 steps (CI = 0.754386, RI = 0.87037, RCI = 0.656595 for all sites and iCI = 0.652174, iRI = 0.870370,

iRCI = 0.567633 for parsimony informative sites). The MP ITS phylogeny grouped all *Gnomoniopsis* isolates from *Castanea* in the same strongly supported clade (MPBS = 99%). The Bayesian distribution of likelihood scores for the ITS dataset was –lnL 1948.241–1998.552 and the PP of the branch supporting the isolates from *Castanea* was strongly supported with a value of 1.00.

Phylogenetic species were characterized using genealogic concordance phylogenetic species recognition (GCPSR) and the genealogical sorting incidence (GSI). The conditional comparison test (GCPSR) was satisfied for the *G. smithogilvyi* clade with MPBS for ITS = 99%, TEF1-α = 100%, β-tubulin = 100%, MS204 = 100% and FG1093 = 100%. Independent marker GSI_T values for *G. smithogilvyi* were all equal to 1 ($p \leq 0.0001–0.0005$), suggesting that this species is a distinct evolutionary lineage from other *Gnomoniopsis* species. The phylogenies of the ITS and five-marker datasets indicate all the isolates associated with *Castanea* represent one species, *G. smithogilvyi.*

Taxonomy

Gnomoniopsis smithogilvyi L.A. Shuttlew., E.C.Y. Liew & D.I. Guest, Persoonia 28: 143. 4 June 2012.

= *Gnomoniopsis castaneae* Tamietti, J. Plant Pathology 94: 416. 21 July 2012, as "*castanea.*"

Specimens examined:

Morphological and molecular examination: **AUSTRALIA**, **New South Wales**, Mullion Creek, 'Brittle Jacks' chestnut orchard, saprobic on dead burrs of *Castanea* sp., Dec. 2009, collected & isolated by L.A. Shuttleworth (holotype CBS H-20623; isotype RBG 5586; ex-type culture CBS 130190 = RBG 5585); Mullion Creek, endophytic in living leaf of *Castanea* sp., Dec 2009, collected & isolated by L.A. Shuttleworth (culture CBS 130189); **Victoria**, Bright, diseased chestnut kernel of *Castanea* sp., April 2009, collected & isolated by L.A. Shuttleworth (culture CBS 130188). **ITALY**, **Piedmont**, Robilante, diseased fruit of *Castanea sativa*, 2007, isolated by G. Tamietti & S. Gentile (culture MUT 401). **NEW ZEALAND**, diseased fruit of *Castanea sativa*, 2007, isolated by H. Smith (culture MUT 411).

Molecular examination only: **FRANCE**, **Picardy**, Oise, stem of *Castanea* sp., 2013, collected by S. Carole (culture LSV 908); **Provence-Alpes-Côte d'Azur**, Sisteron, diseased *Castanea sativa* fruit, 2011, isolated by P. Gonthier & S. Gentile (culture MUT 815). **INDIA**, bark of *Castanea sativa*, collected & isolated by M.A. Dar & M. Rai (culture AU/DBT30); bark of *Castanea sativa*, collected & isolated by M.A. Dar & M. Rai (culture AU/DBT306); on bark of *Castanea sativa*, collected & isolated by M.A. Dar & M. Rai (culture INDC(BSF5)A); bark of *Castanea sativa*, collected & isolated by M.A. Dar & M. Rai (culture AU/DBT296). **ITALY**, **Trentino-South Tyrol**, Val d'Adige, Trento, fruit with brown rot, October 2011 (culture Gn_TN5); **Piedmont**, Val di Susa, Turin, October 2011 (culture Gm_TO); **Tuscany**, Mugello, Florence, October 2011 (culture Gm_FI). **SWITZERLAND**, **Ticino**, Biasca, diseased fruit of *Castanea sativa*, 2011, isolated by M. Jermini (culture MUT 810); **Geneva**, branch wood of *Castanea sativa*, Aug 2013 (culture Ge1, specimen voucher UASWS1319). **NEW ZEALAND**, **Bay of Plenty**, Tauranga, nut of *Castanea sativa*, 1 February 2002, collected by K. Eade (culture ICMP 14492); **Waikato**, nut of *Castanea crenata*, 1 April 2000, isolated

by K.D.R. Wadia (culture ICMP 14080); from *Castanea crenata* × *C. sativa*, isolated by K.D.R. Wadia (culture CBS 121477); from *Castanea* sp., collected & isolated by H. Smith (culture CBS 121917); isolated from *Castanea crenata* (culture CBS 121918).

Ecology & distribution— *Gnomoniopsis smithogilvyi* occurs in Australia on *Castanea sativa* and hybrids of *Castanea crenata* × *C. sativa* (Shuttleworth et al. 2012a,b). In New Zealand it occurs on *C. crenata*, *C. sativa, C. crenata* × *C. sativa* hybrids, and *Castanea* sp.; and in France, India, Italy, and Switzerland on *C. sativa* (Shuttleworth et al. 2012a, Visentin et al. 2012, Maresi et al. 2013). The species is reported as a causal agent of chestnut rot/nut rot in Australia, France, Italy, New Zealand, and Switzerland (Shuttleworth et al. 2012a,b; Visentin et al. 2012), and is reported as the cause of canker of *C. sativa* in India (Dar & Rai 2013, 2015) and Switzerland (Pasche et al. 2015). The fungus is documented as an endophyte of reproductive and vegetative tissues of *C. sativa* in Australia, Italy, and New Zealand, and of *C. crenata* × *C. sativa* hybrids in Australia and New Zealand (Shuttleworth et al. 2012a,b). It also associated with necrosis of leaves and galls induced by *Dryocosmus kuriphilus* (chestnut gall wasp) on *Castanea* spp. in Italy (Magro et al. 2010; Vinale et al. 2014).

Comments— The name *Gnomoniopsis smithogilvyi* was first published on-line on 4 June 2012 in Shuttleworth et al. (2012a). The name *G. castaneae* was first published on-line on 21 July 2012 in Visentin et al. (2012) according to L. Rubino, Editor of the Journal of Plant Pathology (pers. comm.). These on-line publications were both in accordance with Article 29 of the ICN (McNeill et al. 2012). Thus, *G. smithogilvyi* has priority over *G. castaneae*. The earlier informal name, "*Gnomonia pascoe*" was never validly published.

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Literature cited

Bazinet AL, Zwickl DJ, Cummings MP. 2014. A gateway for phylogenetic analysis powered by grid computing featuring GARLI 2.0. Systematic Biology 63(5): 812–818. http://dx.doi.org/10.1093/sysbio/syu031

Barr ME. 1978. The *Diaporthales* in North America with emphasis on *Gnomonia* and its segregates. Mycological Memoirs 7. 232 p.

Bolay A. 1971. Contribution à la connaissance de *Gnomonia comari* Karsten (syn. *G. fructicola* [Arnaud] Fall): étude taxonomique, phytopathologique et recherches sur sa croissance in vitro. Berichte der Schweizerischen Botanischen Gesellschaft 81: 398–482. http://dx.doi.org/10.5169/seals-57134

Carbone I, Kohn LM. 1999. A method for designing primer sets for speciation studies in filamentous ascomycetes. Mycologia 91: 553–556. http://dx.doi.org/10.2307/3761358

Cummings, M.P., Neel, M.C., Shaw, K.L., 2008. A genealogical approach to quantifying lineage divergence. Evolution 62: 2411–2422. http://dx.doi.org/10.1111/j.1558-5646.2008.00442.x

Dar MA, Rai M. 2013. Biological and phylogenetic analyses evidencing the presence of *Gnomoniopsis* sp. in India causing canker of chestnut trees: a new report. Indian Forester 139(1): 37–42.

Dar MA, Rai MK, 2015. *Gnomoniopsis smithogilvyi* a canker causing pathogen on *Castanea sativa*: First report. Mycosphere 6(3): 327–336.

Dennert FG, Broggini GAL, Gessler C, Storari M. 2014. Occurrence of *Gnomoniopsis castanea* [sic] in Switzerland. GenBank accessions: KM437885–KM437892.

Felsenstein J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution 6: 227–242. http://dx.doi.org/10.2307/2408678

Huelsenbeck JP, Ronquist F. 2001. MrBayes: Bayesian inference of phylogeny. Bioinformatics 17: 754–755. http://dx.doi.org/10.1093/bioinformatics/17.8.754

Katoh K, Misawa K, Kuma KI, Miyata T, 2002. MAFFT v7.017. A novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Research 30: 3059–3066. http://dx.doi.org/10.1093/nar/gkf436

Kellogg EA, Appels R, Mason-Gamer RJ. 1996. When genes tell different stories: the diploid genera of *Triticeae* (*Gramineae*). Systematic Botany 21: 321–347.

Maas JL. 1998. Compendium of strawberry diseases. 2nd ed. St Paul, Minnesota: APS Press. 98 p.

Magro P, Speranza S, Stacchiotti M, Martignoni D, Paparatti B. 2010. *Gnomoniopsis* associated with necrosis of leaves and chestnut galls induced by *Dryocosmus kuriphilus*. Plant Pathology 59: 1171. http://dx.doi.org/ 10.1111/j.1365-3059.2010.02336.x

Maresi G, Longa CMO, Turchetti T, 2013. Brown rot on nuts of *Castanea sativa* Mill: an emerging disease and its causal agent. iForest: Biogeosciences and Forestry 6: 294–301. http://dx.doi.org/10.3832/ifor0952-006

Mason-Gamer RJ, Kellogg EA. 1996. Testing for phylogenetic conflict among molecular data sets in the tribe *Triticeae*. Systematic Biology 45: 524–545. http://dx.doi.org/10.1093/sysbio/45.4.524

McNeill J, Barrie FR, Buck WR, Demoulin V, Greuter W, Hawksworth DL, Herendeen PS, Knapp S, Marhold K, Prado J, Prud'homme van Reine WF, Smith GF, Wiersema JH, Turland NJ. 2012. International Code of Nomenclature for algae, fungi, and plants (Melbourne Code) adopted by the Eighteenth International Botanical Congress, Melbourne, Australia, July 2011. Koeltz Scientific Books. http://www.iapt-taxon.org/nomen/main.php

Monod M. 1983. Monographie taxonomique des *Gnomoniaceae* (Ascomycétes de l'ordre des *Diaporthales* I). Beihefte zur Sydowia 9. 315 p.

O'Donnell K, Cigelnik E. 1997. Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. Molecular Phylogenetics & Evolution 7: 103–116. http://dx.doi.org/10.1006/mpev.1996.0376

Pasche S, Calmin G, Crovadore J, Lefort F (2015) Assessment of chestnut canker symptoms showed unexpected evidence for *Gnomoniopsis smithogilvyi* prevalence in *Castanea sativa* shoots in Switzerland. GenBank Accessions: KP824746-KP824755, KP824758-KP824762, KP824764-KP824768.

Posada D. 2008. jModelTest 2.1: Phylogenetic model averaging. Molecular Biology and Evolution 25: 1253–1256. http://dx.doi.org/10.1093/molbev/msn083

Rehner SA. 2001. EF1 alpha primers.
Available at http//ocid.nacse.org/research/deephyphae/EF1primer.pdf

Shuttleworth LA, Liew ECY, Guest DI. 2012a. Fungal Planet description sheet 108: *Gnomoniopsis smithogilvyi* L.A. Shuttleworth, E.C.Y. Liew & D.I. Guest, sp. nov. Persoonia 28: 142–143. http://www.fungalplanet.org/content/pdf-files/FungalPlanet108.pdf

Shuttleworth LA, Liew ECY, Guest DI. 2012b ["2013"]. Survey of the incidence of chestnut rot in south-eastern Australia. Australasian Plant Pathology 42: 63–72. Published online December 2012. http://dx.doi.org/10.1007/s13313-012-0170-2

Smith HC, Ogilvy D. 2008. Nut rot in chestnuts. Scientific research identifies major cause of rot in Australian/New Zealand chestnuts as *Gnomonia pascoe* not *Phomopsis*. Australian Nutgrower 22(2): 10–15.

Sogonov MV, Castlebury LA, Rossman AY, Mejia LC, White JF. 2008. Leaf–inhabiting genera of the *Gnomoniaceae, Diaporthales*. Studies in Mycology 62. 79 p.
http://dx.doi.org/10.3114/sim.2008.62.01

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725–2729. http://dx.doi.org/10.1093/molbev/mst197

Taylor JW, Jacobson DJ, Kroken S, Kasuga T, Geiser DM, Hibbett DS, Fisher MC. 2000. Phylogenetic species recognition and species concepts in fungi. Fungal Genetics and Biology 31(1): 21–32. http://dx.doi.org/10.1006/fgbi.2000.1228

Vinale F, Ruocco M, Manganiello G, Guerrieri E, Bernardo U, Mazzei P, Piccolo A, Sannino F, Caira S, Woo SL, Lorito M. 2014. Metabolites produced by *Gnomoniopsis castanea* [sic] associated with necrosis of chestnut galls. Chemical and Biological Technologies in Agriculture 6: 294–301. http://dx.doi.org/10.1186/s40538-014-0008-y

Visentin I, Gentile S, Valentino D, Gonthier P, Tamietti G, Cardinale F. 2012. *Gnomoniopsis castanea* [sic] sp. nov. (*Gnomoniaceae, Diaporthales*) as a causal agent of nut rot of sweet chestnut. Journal of Plant Pathology 94(2): 411–419.

Walker DM, Castlebury LA, Rossman AY, Sogonov MV, White JF. 2010. Systematics of genus *Gnomoniopsis* (*Gnomoniaceae, Diaporthales*) based on a three-gene phylogeny, host associations and morphology. Mycologia 102(6): 1479–1496. http://dx.doi.org/10.3852/10-002

Walker DM, Castlebury LA, Rossman AY, White JF. 2012. New molecular markers for fungal phylogenetics: Two genes for species-level systematics in the *Sordariomycetes* (*Ascomycota*). Molecular Phylogenetics and Evolution 64: 500–512.
http://dx.doi.org/10.1016/j.ympev.2012.05.005

Zwickl DJ. 2006. Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. Ph.D. dissertation, The University of Texas at Austin.